SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
                Lal, Preeti
                Corley, Neil C.
                Shah, Purvi

(ii) TITLE OF THE INVENTION: HUMAN CITRATE SYNTHASE HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  (B) STREET: 3174 Porter Drive
  (C) CITY: Palo Alto
  (D) STATE: CA
  (E) COUNTRY: USA
  (F) ZIP: 94304

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER: To Be Assigned
  (B) FILING DATE: Herewith
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Billings, Lucy J.
  (B) REGISTRATION NUMBER: 36,749
  (C) REFERENCE/DOCKET NUMBER: PF-0425 US

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 650-855-0555
  (B) TELEFAX: 650-845-4166
  (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 466 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
  (A) LIBRARY: ENDCNOT03
  (B) CLONE: 2171653

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Leu Leu Thr Ala Ala Ala Arg Leu Leu Gly Thr Lys Asn Ala
1               5                   10                  15
Ser Cys Leu Val Leu Ala Ala Arg His Ala Ser Ala Ser Ser Thr Asn
                20                  25                  30
Leu Lys Asp Ile Leu Ala Asp Leu Ile Pro Lys Glu Gln Ala Arg Ile
        35                  40                  45
Lys Thr Phe Arg Gln Gln His Gly Lys Thr Val Val Gly Gln Ile Thr
    50                  55                  60
Val Asp Met Met Tyr Gly Gly Met Arg Gly Met Lys Gly Leu Val Tyr
65                  70                  75                  80
Glu Thr Ser Val Leu Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Phe
                85                  90                  95
Ser Ile Pro Glu Cys Gln Lys Leu Leu Pro Lys Ala Lys Gly Gly Glu
            100                 105                 110
Glu Pro Leu Pro Glu Gly Leu Phe Trp Leu Leu Val Thr Gly His Ile
        115                 120                 125
Pro Thr Glu Glu Gln Val Ser Trp Leu Ser Lys Glu Trp Ala Lys Arg
    130                 135                 140
Ala Ala Leu Pro Ser His Val Val Thr Met Leu Asp Asn Phe Pro Thr
145                 150                 155                 160
Asn Leu His Pro Met Ser Gln Leu Ser Ala Ala Val Thr Ala Leu Asn
                165                 170                 175
Ser Glu Ser Asn Phe Ala Arg Ala Tyr Ala Gln Gly Ile Ser Arg Thr
            180                 185                 190
Lys Tyr Trp Glu Leu Ile Tyr Glu Asp Ser Met Asp Leu Ile Ala Lys
    195                 200                 205
Leu Pro Cys Val Ala Ala Lys Ile Tyr Arg Asn Leu Tyr Arg Glu Gly
    210                 215                 220
Ser Gly Ile Gly Ala Ile Asp Ser Asn Leu Asp Trp Ser His Asn Phe
225                 230                 235                 240
Thr Asn Met Leu Gly Tyr Thr Asp His Gln Phe Thr Glu Leu Thr Arg
                245                 250                 255
Leu Tyr Leu Thr Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala
                260                 265                 270
His Thr Ser His Leu Val Gly Ser Ala Leu Ser Asp Pro Tyr Leu Ser
    275                 280                 285
Phe Ala Ala Ala Met Asn Gly Leu Ala Gly Pro Leu His Gly Leu Ala
    290                 295                 300
Asn Gln Glu Val Leu Val Trp Leu Thr Gln Leu Gln Lys Glu Val Gly
305                 310                 315                 320
Lys Asp Val Ser Asp Glu Lys Leu Arg Asp Tyr Ile Trp Asn Thr Leu
                325                 330                 335
Asn Ser Gly Arg Val Val Pro Gly Tyr Gly His Ala Val Leu Arg Lys
            340                 345                 350
Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu Phe Ala Leu Lys His Leu
        355                 360                 365
Pro Asn Asp Pro Met Phe Lys Leu Val Ala Gln Leu Tyr Lys Ile Val
    370                 375                 380
Pro Asn Val Leu Leu Glu Gln Gly Lys Ala Lys Asn Pro Trp Pro Asn
385                 390                 395                 400
Val Asp Ala His Ser Gly Val Leu Leu Gln Tyr Tyr Gly Met Thr Glu
                405                 410                 415
Met Asn Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg Ala Leu Gly Val
            420                 425                 430
Leu Ala Gln Leu Ile Trp Ser Arg Ala Leu Gly Phe Pro Leu Glu Arg
        435                 440                 445
Pro Lys Ser Met Ser Thr Glu Gly Leu Met Lys Phe Val Asp Ser Lys
    450                 455                 460
```

2

Ser Gly
465

```
        (2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2131 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
        (A) LIBRARY: ENDCNOT03
        (B) CLONE: 2171653

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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CGCCGGTTCG TCTACTCTTT CCTTCAGCCG CCTCCTTTCA ACCTTGTCAA CCCGTCGGCG      60
CGGCCTCTGG TGCAGCGGCG GCGGCTCCTG TTCCTGCCGC AGCTCTCTCC CTTTCTTACC     120
TCCCCACCAG ATCCCGGAGA TCGCCCGCCA TGGCTTTACT TACTGCGGCC GCCCGGCTCT     180
TGGGAACCAA GAATGCATCT TGTCTTGTTC TTGCAGCCCG GCATGCCAGT GCTTCCTCCA     240
CGAATTTGAA AGACATATTG GCTGACCTGA TACCTAAGGA GCAGGCCAGA ATTAAGACTT     300
TCAGGCAGCA ACATGGCAAG ACGGTGGTGG GCCAAATCAC TGTGGACATG ATGTATGGTG     360
GCATGAGAGG CATGAAGGGA TTGGTCTATG AAACATCAGT TCTTGATCCT GATGAGGGCA     420
TCCGTTTCCG AGGCTTTAGT ATCCCTGAAT GCCAGAAACT GCTACCCAAG GCTAAGGGTG     480
GGGAAGAACC CCTGCCTGAG GGCTTATTTT GGCTGCTGGT AACTGGACAT ATCCCAACAG     540
AGGAACAGGT ATCTTGGCTC TCAAAAGAGT GGGCAAAGAG GGCAGCTCTG CCTTCCCATG     600
TGGTCACCAT GCTGGACAAC TTTCCCACCA ATCTACACCC CATGTCTCAG CTCAGTGCAG     660
CTGTTACAGC CCTCAACAGT GAAAGTAACT TTGCCCGAGC ATATGCACAG GGTATCAGCC     720
GAACCAAGTA CTGGGAGTTG ATTTATGAAG ACTCTATGGA TCTAATCGCA AAGCTACCTT     780
GTGTTGCAGC AAAGATCTAC CGAAATCTCT ACAGAGAAGG CAGCGGTATT GGGGCCATTG     840
ACTCTAACCT GGACTGGTCT CACAATTTCA CCAACATGTT AGGCTATACT GATCATCAGT     900
TCACTGAGCT CACGCGCCTG TACCTCACCA TCCACAGTGA CCATGAGGGT GGCAATGTAA     960
GTGCCCATAC CAGCCATTTG GTGGGCAGTG CCCTTTCCGA CCCTTACCTG TCCTTTGCAG    1020
CAGCCATGAA CGGGCTGGCA GGGCCTCTCC ATGGACTGGC AAATCAGGAA GTGCTTGTCT    1080
GGCTAACACA GCTGCAGAAC GAAGTTGGCA AAGATGTGTC AGATGAGAAG TTACGAGACT    1140
ACATCTGGAA CACACTCAAC TCAGGACGGG TTGTTCCAGG CTATGGCCAT GCAGTACTAA    1200
GGAAGACTGA TCCGCGATAT ACCTGTCAGC GAGAGTTTGC TCTGAAACAC CTGCCTAATG    1260
ACCCCATGTT TAAGTTGGTT GCTCAGCTGT ACAAGATTGT GCCCAATGTC CTCTTAGAGC    1320
AGGGTAAAGC CAAGAATCCT TGGCCCAATG TAGATGCTCA CAGTGGGGTG CTGCTCCAGT    1380
ATTATGGCAT GACGGAGATG AATTACTACA CGGTCCTGTT TGGGGTGTCA CGAGCATTGG    1440
GTGTACTGGC ACAGCTCATC TGGAGCCGAG CCTTAGGCTT CCCTCTAGAA AGGCCCAAGT    1500
CCATGAGCAC AGAGGGTCTG ATGAAGTTTG TGGACTCTAA GTCAGGGTAA AACTGGAGAC    1560
TGGGTGAAAG TGACTACCAG AAAGTGAGGA AGCCTAAATA AAAAGTATAC TTTTGTTTCA    1620
GGGGGGCCTTT AAAGACTTAA GATTAAATTA TATCTGAGGC ACTGATAATA TGTTTGAGGT    1680
TAAAATATAA ATTAAGACTT TAAAAGATGA AAAATGGTCC CTTCTTCCCT AATCAGCTCC    1740
CTTCCCCTGC CTGGTATGAG TTGCCCATCA TACGCATGGT CCTGGAGGAT GACCAGGACT    1800
AATGCATGTG GTATGAGTAG GTTTGGCCCC CTCACTATCT CTAGAGTGAG AATCTGGCTC    1860
CTGTTTCCAT GGGTCAAAGC CGGTTGCAGA GAATCTGTAG TCACTTTGGA GCTTTAGCTT    1920
CTCTGCCAAG CCCTCAATAA GCCAGCAAAC CAGGACTCTG CCCCTTCTGT TTCCATAGGA    1980
ATCATGTTGG ATAGTCAGCT GTACCAAGCC CCTTGGCCCT CTCCCATGCA CACAAACACC    2040
TCCTAGCAAG ACCTGTTGGT TAGCTGGACA TGCTTTGGCA ATTTTTTTAT ACTACCAAGT    2100
GACCATATTG GCATGGCATT TTTTGGTGAT G                                   2131
```

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        (2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 464 amino acids
        (B) TYPE: amino acid
```

3

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
  (A) LIBRARY: GenBank
  (B) CLONE: 164419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Ala Leu Leu Thr Ala Ala Ala Arg Leu Phe Gly Ala Lys Asn Ala
1               5                   10                  15
Ser Cys Leu Val Leu Ala Ala Arg His Ala Ser Ala Ser Ser Thr Asn
            20                  25                  30
Leu Lys Asp Ile Leu Ala Asp Leu Ile Pro Lys Glu Gln Ala Arg Ile
        35                  40                  45
Lys Thr Phe Arg Gln Gln His Gly Asn Thr Val Val Gly Gln Ile Thr
    50                  55                  60
Val Asp Met Met Tyr Gly Gly Met Arg Gly Met Lys Gly Leu Val Tyr
65                  70                  75                  80
Glu Thr Ser Val Leu Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Tyr
                85                  90                  95
Ser Ile Pro Glu Cys Gln Lys Met Leu Pro Lys Ala Lys Gly Gly Glu
            100                 105                 110
Glu Pro Leu Pro Glu Gly Leu Phe Trp Leu Leu Val Thr Gly Gln Ile
        115                 120                 125
Pro Thr Glu Glu Gln Val Ser Trp Leu Ser Lys Glu Trp Ala Lys Arg
    130                 135                 140
Ala Ala Leu Pro Ser His Val Val Thr Met Leu Asp Asn Phe Pro Thr
145                 150                 155                 160
Asn Leu His Pro Met Ser Gln Leu Ser Ala Ala Ile Thr Ala Leu Asn
                165                 170                 175
Ser Glu Ser Asn Phe Ala Arg Ala Tyr Ala Glu Gly Ile His Arg Thr
            180                 185                 190
Lys Tyr Trp Glu Leu Ile Tyr Glu Asp Cys Met Asp Leu Ile Ala Lys
            195                 200                 205
Leu Pro Cys Val Ala Ala Lys Ile Tyr Arg Asn Leu Tyr Arg Glu Gly
    210                 215                 220
Ser Ser Ile Gly Ala Ile Asp Ser Lys Leu Asp Trp Ser His Asn Phe
225                 230                 235                 240
Thr Asn Met Leu Gly Tyr Thr Asp Ala Gln Phe Thr Glu Leu Met Arg
                245                 250                 255
Leu Tyr Leu Thr Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala
            260                 265                 270
His Thr Ser His Leu Val Gly Ser Ala Leu Ser Asp Pro Tyr Leu Ser
            275                 280                 285
Phe Ala Ala Ala Met Asn Gly Leu Ala Gly Pro Leu His Gly Leu Ala
    290                 295                 300
Asn Gln Glu Val Leu Val Trp Leu Thr Gln Leu Gln Lys Glu Val Gly
305                 310                 315                 320
Lys Asp Val Ser Asp Glu Lys Leu Arg Asp Tyr Ile Trp Asn Thr Leu
                325                 330                 335
Asn Ser Gly Arg Val Val Pro Gly Tyr Gly His Ala Val Leu Arg Lys
            340                 345                 350
Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu Phe Ala Leu Lys His Leu
            355                 360                 365
Pro His Asp Pro Met Phe Lys Leu Val Ala Gln Leu Tyr Lys Ile Val
    370                 375                 380
Pro Asn Val Leu Leu Glu Gln Gly Lys Ala Lys Asn Pro Trp Pro Asn
385                 390                 395                 400
Val Asp Ala His Ser Gly Val Leu Leu Gln Tyr Tyr Gly Met Thr Glu
```

4

```
                    405                      410                      415
 Met Asn Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg Ala Leu Gly Val
             420                      425                      430
 Leu Ala Gln Leu Ile Trp Ser Arg Ala Leu Gly Phe Pro Leu Glu Arg
         435                      440                      445
 Pro Lys Ser Met Ser Thr Asp Gly Leu Ile Lys Leu Val Asp Ser Lys
     450                      455                      460
```